REMARKS

I. Status of the Claims

Claims 1-88 were originally filed. Claims 6, 20-69, 71, 76-82, and 84 have been canceled. Claims 1-5, 7-19, 70, 72-75, 83, and 85-88 are pending under examination.

Upon entry of the present amendment, claim 5 is amended to recite "wherein the amino acid at position 577 has been substituted by a different amino acid." This amendment does not introduce new matter, since position 577 in SEQ ID NO:20 corresponds to position 208 in SEQ ID NO:2 and position 183 in SEQ ID NO:4 (see Exhibit 1). Claim 13 is amended to add the missing space between "of" and "MTB8.4." Claim 83 is amended to recite an "isolated fusion polypeptide" instead of an "isolated polypeptide encoding a fusion polypeptide." This amendment merely corrects a grammatical error and introduces no new matter.

III. Claim Rejections

A. Double Patenting

Claims 1, 4, 5, and 19 were rejected under the judicially created doctrine of obviousness-type of double patenting over claim 1 of U.S. Patent No. 6,627,198. Applicants respectfully traverse the rejection in light of the present amendment.

Claim 1 of U.S. Patent No. 6,627,198 ("the '198 patent") is drawn to a purified polypeptide comprising the amino acid sequence of SEQ ID NO:26, which is identical to SEQ ID NO:20 of the present application. Following the amendment of November 22, 2004, claim 1 recites "at least one amino acid corresponding to position 183 of SEQ ID NO:4 or position 208 of SEQ ID NO:2 in the MTB32A antigen (SEQ ID NO:2 or 4) has been substituted by a different amino acid." As indicated in Exhibit 1, it is clear that SEQ ID NO:20 of the present invention (or SEQ ID NO:26 of the '198 patent) contains a partial sequence of SEQ ID NO:2 or SEQ ID NO:4, including position 208 of SEQ ID NO:2 or position 183 of SEQ ID NO:4, which is a serine and corresponds to position 577 in SEQ ID NO:20. Thus, the limitation that at least one of these two positions is substituted with a different amino acid requires claim 1 to exclude SEQ

ID NO:20, when position 577 remains a serine. For this reason, claims 1, 4, and 19 are not obvious over claim 1 of the '198 patent.

Upon entry of the present amendment, claim 5 is further amended to recite "wherein the amino acid at position 577 has been substituted by a different amino acid." This newly added limitation explicitly distinguishes the fusion polypeptide in the claimed composition from SEQ ID NO:26 of the '198 patent. Thus, the amended claim 5 is not obvious over claim 1 of the '198 patent.

Accordingly, the withdrawal of the double patenting rejection is respectfully requested.

B. 35 U.S.C. §112, Second Paragraph

The Examiner also rejected claim 83 and 85-87 were rejected under 35 U.S.C. §112, second paragraph, for indefiniteness. Specifically, the Examiner pointed to the language in claim 83 reciting an "isolated polypeptide encoding a fusion polypeptide." Following the present amendment, claim 83 new recites an "isolated fusion polypeptide" in place of the original phrase. Thus, the indefiniteness rejection of claim 83 and its dependent claims is obviated.

III. Claim Objections

Claims 2, 3, and 7-18 were objected to for their dependency from rejected base claims. As discussed above, all claim rejections have now been properly addressed. Thus, the objection of these claims for depending from rejected base claims is moot.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,

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Reg. No. 54,111

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Attachment (Exhibit 1: SEQ ID NO:2, SEQ ID NO:4, and SEQ ID NO:20, marked up to show correspondence)
CG:cg
60486599 v1

INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: MTB32A (Ra35FL)

```
Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
1               5                  10                  15
Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
            20                  25                  30
Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
        35                  40                  45
Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
    50                  55                  60
Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
65                  70                  75                  80
Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
                85                  90                  95
Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
            100                 105                 110
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
        115                 120                 125
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
    130                 135                 140
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
145                 150                 155                 160
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
                165                 170                 175
Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
            180                 185                 190
Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
        195                 200                 205
Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
    210                 215                 220
Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
225                 230                 235                 240
Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
                245                 250                 255
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
            260                 265                 270
Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
        275                 280                 285
Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
    290                 295                 300
Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
305                 310                 315                 320
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
                325                 330                 335
Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
            340                 345                 350
Pro Pro Ala
        355
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<213> Ra35 mature
<400> SEQ ID NO:4

402 in NO: 20

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             20                  25                  30

Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
         35                  40                  45

Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
     50                  55                  60

Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
 65                  70                  75                  80

Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
                 85                  90                  95

Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
            100                 105                 110

Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val
        115                 120                 125

Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
    130                 135                 140

Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
145                 150                 155                 160

Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
                165                 170                 175

Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly
            180                 185                 190

Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
        195                 200                 205

Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
    210                 215                 220

Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly
225                 230                 235                 240

Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
                245                 250                 255

Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
            260                 265                 270

Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
        275                 280                 285

Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
    290                 295                 300

Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
305                 310                 315                 320

Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
                325                 330
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NO:20 (596)

<210> SEQ ID NO:20
<211> 596
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:bi-fusion protein TbH9-Ra35 (designated Mtb59f)

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Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
             20                  25                  30

Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
         35                  40                  45

Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
     50                  55                  60

Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
 65                  70                  75                  80

Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
                 85                  90                  95

Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
            100                 105                 110

Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
        115                 120                 125

Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
    130                 135                 140

Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
145                 150                 155                 160

Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
                165                 170                 175

Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
            180                 185                 190

Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
        195                 200                 205

Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
    210                 215                 220

Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
225                 230                 235                 240
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
                245                 250                 255

Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
            260                 265                 270

Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr
        275                 280                 285

Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
    290                 295                 300

Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
305                 310                 315                 320

Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn
                325                 330                 335
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Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr
340 345 350

Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val
355 360 365

Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg
370 375 380

Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp
385 390 395 400

Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala
405 410 415

Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val
420 425 430

Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly
435 440 445

Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His
450 455 460

Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly
465 470 475 480

Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val
485 490 495

Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile
500 505 510

Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser
515 520 525

Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala
530 535 540

Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu
545 550 555 560

Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp
565 570 575

Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn
580 585 590

Thr Ala Ala Ser
595

NO:14

33 in NO: 2; 8 in NO: 4

227 in NO: 2
202 in NO: 4